

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) TITLE OF INVENTION: A VACCINE-INDUCED HEPATITIS B VIRAL STRAIN AND USES THEREOF

(ii) NUMBER OF SEQUENCES: 11

## (2) INFORMATION FOR SEQ ID NO:1: (Figure 3)

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACCACT TTCCACCAA CTCTTCAAGA TCCCAGAGTC AGGGCCCTGT ACTTTCCTGC	60
TGGTGGCTCC AGTTCAGGAA CAGTGAGCCC TGCTCAGAAT ACTGTCTCTG CCATATCGTC	120
AATCTTATCG AAGACTGGGG ACCCTGTACC GAACATGGAG AACATCGCAT CAGGACTCCT	180
AGGACCCCTG CTCGTGTTAC AGGCGGGGTT TTTCTTGTTG AAAAAATCC TCACAATACC	240
GCAGAGTCTA GACTCGTGGT GGACTTCTCT CAATTTTCTA GGGGGAACAC CCGTGTGTCT	300
TGGCCAAAAT TCGCAGTCCC AAATCTCCAG TCACTCACCA ACCTGTTGTC CTCCAATTTG	360
TCCTGGTTAT CGCTGGATGT GTCTGCGGCG TTTTATCATC TTCCTCTGCA TCCTGCTGCT	420
ATGCCATCATC TTCTTGTTGG TTCTTCTGGA CTATCAAGGT ATGTTGCCCG TTTGTCTCT	480
AATTCCAGGA TCAACAACAA CCAGCACCGG ACCATGCAA ACCTGCACAA CTCCTGCTCA	540
AGGAACCTCT ATGTTTCCCT CATGTTGCTG TACAAAACCT ACGGACAGAA ACTGCACCTG	600
TATTCCCATC CCATCATCTT GGGCTTTTCG AAAATACCTA TGGGAGTGGG CCTCAGTCCG	660
TTTCTCTTGG CTCAGTTTAC TAGTGCCATT TGTTCACTGG TTCGTAGGGC TTTCCCCAC	720
TGTCTGGCTT TCAGTTATAT GGATGATGTG GTTTTGGGG CCAAGTCTGT ACAACATCTT	780
GAGTCCCTTT ATGCCGCTGT TACCAATTTT CTTTGTCTT TGGGTATACA TTTAAACCCT	840
CACAAAACAA AAAGATGGGG ATATTCCCTT AACTTCATGG GATATGTCAT TGGGAGTTGG	900
GGCACATTGC CACAGGAACA TATTGTACAA AAAATCAAAA TGTGTTTTAG GAAACTTCCT	960
GTAAACAGGC CTATTGATTG GAAAGTATGT CAACGAATTG TGGGTCTTTT GGGGTTTGCC	1020
GCCCCTTTCA CGCAATGTGG ATATCCTGCT TTAATGCCTT TATATGCATG TATACAAGCA	1080
AAACAGGCTT TTAATTTCTC GCAAACTTAC AAGACCTTTC TAAGTAAACA GTATCTGAAC	1140
CTTTACCCCG TTGCTCGGCA ACGCCCTGGT CTGTGCCAAG TGTTTGCTGA CGCAACCCCC	1200
ACTGGTTGGG GCTTGGCCAT AGGCCATCAG CGCATGCGTG GAACCTTTGT GTCTCCTCTG	1260

CCGATCCATA	CTGCGGAACT	CCTAGCCGCT	TGTTTTGCTC	GCAGCAGGTC	TGGGGCAAAA	1320
CTCATCGGGA	CTGACAATTC	TGTCGTGCTC	TCCCCGAACT	ATACATCATT	TCCATGGCTG	1380
CTAGGCTGTG	CTGCCAACTG	GATCCTGCGC	GGGACGTCCT	TTGTTTACGT	CCCGTCGGCG	1440
CTGAATCCCG	CGGACGACCC	CTCCCGGGGC	CGCTTGGGGC	TCTACCGCCC	GCTTCTCCGC	1500
CTGTTATACC	GACCGACCAC	GGGGCGCACC	TCTCTTTACG	CGGACTCCCC	GTCTGTGCCT	1560
TCTCATCTGC	CGGACCGTGT	GCACTTCGCT	TCACCTCTGC	ACGTCGCATG	GAGACCACCG	1620
TGAACGCCCC	CGGGAACCTG	CCCAAGGTCT	TGCATAAGAG	GACTCTTGGA	CTTTCAGCAA	1680
TGTCAACGAC	CGACCTTGAG	GCATACTTCA	AAGACTGTGT	GTTTAATGAG	TGGGAGGAGT	1740
TGGGGGAGGA	GGTTAGGTTA	AAGGTCTTTG	TACTAGGAGG	CTGTAGGCAT	AAATTGGTGT	1800
GTTCAACATC	ACCATGCAAC	TTTTTCACCT	CTGCCTAATC	ATCTCATGTT	CATGTCCTAC	1860
TGTTCAAGCC	TCCAAGCTGT	GCCTTGGGTG	GCTTTGGGGC	ATGGACATTG	ACCCGTATAA	1920
AGAATTTGGA	GCTTCTGTGG	AGTTACTCTC	TTTTTTGCCT	TCTGACTTTT	TTCTTCTAT	1980
TCGAGATCTC	CTCGACACCG	CCTCTGCTCT	GTATCGGGAG	GCCTTAGAGT	CTCCGGAACA	2040
TTGTTACCT	CACCATACGG	CACTCAGGCA	AGCTATTCTG	AGTTGGGGTG	AGTTAATGAA	2100
TCTAGCCACC	TGGGTGGGAA	GTAATTTGGA	AGATCCAGCA	TCCAGGGAAT	TAGTAGTCAG	2160
CTATGTCAAC	GTTAATATGG	GCCTAAAAAT	CAGACAACTA	TTGTGGTTTC	ACATTTCTCTG	2220
TCTTACTTTT	GGGAGAGAAA	CTGTTCTTGA	ATATTTGGTG	TCTTTTGGAG	TGTGGATTCTG	2280
CACTCCTCCT	GCATATAGAC	CACCAAATGC	CCCTATCTTA	TCAACACTTC	CGGAAACTAC	2340
TGTTGTTAGA	CGAAGAGGCA	GGTCCCCTAG	AAGAAGAACT	CCCTCGCCTC	GCAGACGAAG	2400
GTCTCAATCG	CCGCGTCGCA	GAAGATCTCA	ATCTCGGGAA	TCTCAATGTT	AGTATTCCTT	2460
GGACACATAA	GGTGGGAAAC	TTTACGGGGC	TTTATTCTTC	TACGGTACCT	TGCTTTAATC	2520
CTAAATGGCA	AACTCCTTCT	TTTCCGGACA	TTTATTGCA	GGAGGACATT	CTTGATAGAT	2580
GTAAGCAATT	TGTGGGGCCC	CTTACAGTAA	ATGAAAACAG	GAGACTAAAA	TTAATTATGC	2640
CTGCTAGGTT	TTATCCAAAT	GTTACTAAAT	ATTTGCCCTT	AGATAAAGGG	ATCAAACCAT	2700
ATTATCCAGA	GTATGTAGTT	AATCATTACT	TCCAGACGCG	ACATTATTTA	CACACTCTTT	2760
GGAAGGCGGG	GATCTTATAT	AAAAGAGAGT	CCACACGTAG	CGCCTCATTT	TGCGGGTCAC	2820
CATATTCTTG	GGAACAAGAT	CTACAGCATG	GGAGGTGGT	CTTCCAAACC	TCGAAAAGGC	2880
ATGGGGACAA	ATCTTTCTGT	CCCCAATCCC	CTGGGATTCT	TCCCCGATCA	TCAGTTGGAC	2940
CCTGCATTCA	AAGCCAACTC	AGAAAATCCA	GATTGGGACC	TCAACCCGCA	CAAGGACAAC	3000
TGGCCGGACG	CCAACAAGGT	GGGAGTGGGA	GCATTCGGGC	CAGGGTTCAC	CCCTCCTCAT	3060
GGGGGACTGT	TGGGGTGGAG	CCCTCAGGCT	CAGGGCCTAC	TCACAACTGT	GCCAGCAGCT	3120
CCTCCTCCTG	CCTCCACCAA	TCGGCAGTCA	GGAAGGCAGC	CTACTCCCTT	ATCTCCACCT	3180
CTAAGGGACA	CTCATCCTCA	GGCCATGCAG	TGGAA			3215

## (2) INFORMATION FOR SEQ ID NO:2: (Figure 4)

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Glu
1          5          10          15
Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
20          25          30
Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35          40          45
Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
50          55          60
Ser Thr Val Pro Cys Phe Asn Pro Lys Trp Gln Thr Pro Ser Phe Pro
65          70          75          80
Asp Ile His Leu Gln Glu Asp Ile Leu Asp Arg Cys Lys Gln Phe Val
85          90          95
Glu Pro Leu Thr Val Asn Glu Asn Arg Arg Leu Lys Leu Ile Met Pro
100         105         110
Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115         120         125
Ile Lys Pro Tyr Tyr Pro Glu Tyr Val Val Asn His Tyr Phe Gln Thr
130         135         140
Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145         150         155         160
Glu Ser Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165         170         175
Gln Asp Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Lys Arg His
180         185         190
Gly Asp Lys Ser Phe Cys Pro Glu Ser Pro Gly Ile Leu Pro Arg Ser
195         200         205
Ser Val Gly Pro Cys Ile Gln Ser Gln Leu Arg Lys Ser Arg Leu Gly
210         215         220
Pro Gln Pro Ala Gln Gly Gln Leu Ala Gly Arg Gln Gln Gly Gly Ser
225         230         235         240
Gly Ser Ile Arg Ala Arg Val His Pro Ser Ser Trp Gly Thr Val Gly
245         250         255
Val Glu Pro Ser Gly Ser Gly Pro Thr His Asn Cys Ala Ser Ser Ser
260         265         270
Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser Leu
275         280         285

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Ile Ser Thr Ser Lys Gly His Ser Ser Ser Gly His Ala Val Glu Leu  
 290 295 300  
 His His Phe Pro Pro Asn Ser Ser Arg Ser Gln Ser Gln Gly Pro Val  
 305 310 315 320  
 Leu Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Glu Pro Cys Ser Glu  
 325 330 335  
 Tyr Cys Leu Cys His Ile Val Asn Leu Ile Glu Asp Trp Gly Pro Cys  
 340 345 350  
 Thr Glu His Gly Glu His Arg Ile Arg Thr Pro Arg Thr Pro Ala Arg  
 355 360 365  
 Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala  
 370 375 380  
 Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Thr  
 385 390 395 400  
 Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr  
 405 410 415  
 Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala  
 420 425 430  
 Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu  
 435 440 445  
 Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn  
 450 455 460  
 Ser Arg Ile Asn Asn Asn Glu His Arg Thr Met Glu Asn Leu His Asn  
 465 470 475 480  
 Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr  
 485 490 495  
 Tyr Gly Gln Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe  
 500 505 510  
 Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln  
 515 520 525  
 Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys  
 530 535 540  
 Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val  
 545 550 555 560  
 Gln His Leu Glu Ser Leu Tyr Ala Ala Val Thr Asn Phe Leu Leu Ser  
 565 570 575  
 Leu Gly Ile His Leu Asn Pro His Lys Thr Lys Arg Trp Gly Tyr Ser  
 580 585 590  
 Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln  
 595 600 605  
 Glu His Ile Val Gln Lys Ile Lys Met Cys Phe Arg Lys Leu Pro Val  
 610 615 620  
 Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu  
 625 630 635 640

Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro  
                                 645                                650                                655  
 Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser Gln Thr  
                                 660                                665                                670  
 Tyr Lys Thr Phe Leu Ser Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala  
                                 675                                680                                685  
 Arg Gln Arg Pro Gly Leu Cys Glu Val Phe Ala Asp Ala Thr Pro Thr  
                                 690                                695                                700  
 Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Thr Phe Val  
                                 705                                710                                715                                720  
 Ser Pro Leu Pro Ile His Thr Ala Glu Leu Leu Ala Ala Cys Phe Ala  
                                 725                                730                                735  
 Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val  
                                 740                                745                                750  
 Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala  
                                 755                                760                                765  
 Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu  
                                 770                                775                                780  
 Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro  
                                 785                                790                                795                                800  
 Leu Leu Arg Leu Leu Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr  
                                 805                                810                                815  
 Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe  
                                 820                                825                                830  
 Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro  
                                 835                                840

## (2) INFORMATION FOR SEQ ID NO:3: (Figure 5)

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu  
 1                                5                                10                                15  
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro  
                                 20                                25                                30  
 Ala Phe Lys Ala Asn Ser Glu Asn Pro Asp Trp Asp Leu Asn Pro His  
                                 35                                40                                45  
 Lys Asp Asn Trp Pro Asp Ala Asn Lys Val Gly Val Gly Ala Phe Gly  
                                 50                                55                                60  
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln  
                                 65                                70                                75                                80

Ala Gln Gly Leu Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser  
 85 90 95  
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu  
 100 105 110  
 Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His  
 115 120 125  
 Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly  
 130 135 140  
 Gly Ser Ser Ser Gly Thr Val Ser Pro Ala Gln Asn Thr Val Ser Ala  
 145 150 155 160  
 Ile Ser Ser Ile Leu Ser Lys Thr Gly Asp Pro Val Pro Asn Met Glu  
 165 170 175  
 Asn Ile Ala Ser Gly Leu Leu Gly Pro Leu Leu Val Leu Gln Ala Gly  
 180 185 190  
 Phe Phe Leu Leu Thr Lys Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
 195 200 205  
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Pro Thr Val Cys Leu Gly  
 210 215 220  
 Gln Asn Ser Gln Ser Gln Ile Ser Ser His Ser Pro Thr Cys Cys Pro  
 225 230 235 240  
 Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile  
 245 250 255  
 Phe Leu Cys Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu  
 260 265 270  
 Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Thr  
 275 280 285  
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly  
 290 295 300  
 Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp Arg Asn  
 305 310 315 320  
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys Tyr Leu  
 325 330 335  
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro  
 340 345 350  
 Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val  
 355 360 365  
 Ile Trp Met Met Trp Phe Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser  
 370 375 380  
 Pro Phe Met Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile  
 385 390 395 400

## (2) INFORMATION FOR SEQ ID NO:4: (Figure 6)

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1           5           10
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20           25           30
Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu Ser Phe Leu
35           40           45
Pro Ser Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp Thr Ala Ser
50           55           60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65           70           75           80
His Thr Ala Leu Arg Gln Ala Ile Leu Ser Trp Gly Glu Leu Met Asn
85           90           95
Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala Ser Arg Glu
100          105          110
Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Ile Arg Gln
115          120          125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130          135          140
Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145          150          155          160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165          170          175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180          185          190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195          200          205
Glu Ser Gln Cys
210

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## (2) INFORMATION FOR SEQ ID NO:5: (Figure 7)

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ala Arg Leu Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu  
 1 5 10 15  
 Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Leu Pro Gly  
 20 25 30  
 Pro Leu Gly Ala Leu Pro Pro Ala Ser Pro Pro Val Ile Pro Thr Asp  
 35 40 45  
 His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser  
 50 55 60  
 Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu  
 65 70 75 80  
 Thr Thr Val Asn Ala His Gly Asn Leu Pro Lys Val Leu His Lys Arg  
 85 90 95  
 Thr Leu Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe  
 100 105 110  
 Lys Asp Cys Val Phe Asn Glu Trp Glu Glu Leu Gly Glu Glu Val Arg  
 115 120 125  
 Leu Lys Val Phe Val Leu Gly Gly Cys Arg His Lys Leu Val Cys Ser  
 130 135 140  
 Pro Ser Pro Cys Asn Phe Phe Thr Ser Ala  
 145 150

## (2) INFORMATION FOR SEQ ID NO:6: (Figure 8)

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTATG CCCCTATCTT ATCAACACTT CCGGA

35

## (2) INFORMATION FOR SEQ ID NO:7: (Figure 9)

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA

25



## (2) INFORMATION FOR SEQ ID NO:8: (Figure 10)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGA CTTCT

25

## (2) INFORMATION FOR SEQ ID NO:9: (Figure 11)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

## (2) INFORMATION FOR SEQ ID NO:10: (Figure 12)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

## (2) INFORMATION FOR SEQ ID NO:11: (Figure 13)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGCTTAG TTTCCGGAAG TGTTGAT

27